# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 18:36:27*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084867.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3084867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084867.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 18:36:26 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3084867.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,705,038 |
| Mapped reads | 2,421,321 / 89.51% |
| Unmapped reads | 283,717 / 10.49% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 18,403 / 0.68% |
| Read min/max/mean length | 30 / 76 / 76.24 |
| Duplicated reads (estimated) | 106,697 / 3.94% |
| Duplication rate | 3.69% |
| Clipped reads | 801,678 / 29.64% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 49,350,000 / 29.34% |
| Number/percentage of C's | 30,765,382 / 18.29% |
| Number/percentage of T's | 53,969,701 / 32.09% |
| Number/percentage of G's | 34,063,387 / 20.25% |
| Number/percentage of N's | 26,284 / 0.02% |
| GC Percentage | 38.55% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0543 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4108 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.68 |

## 2.5. Mismatches and indels

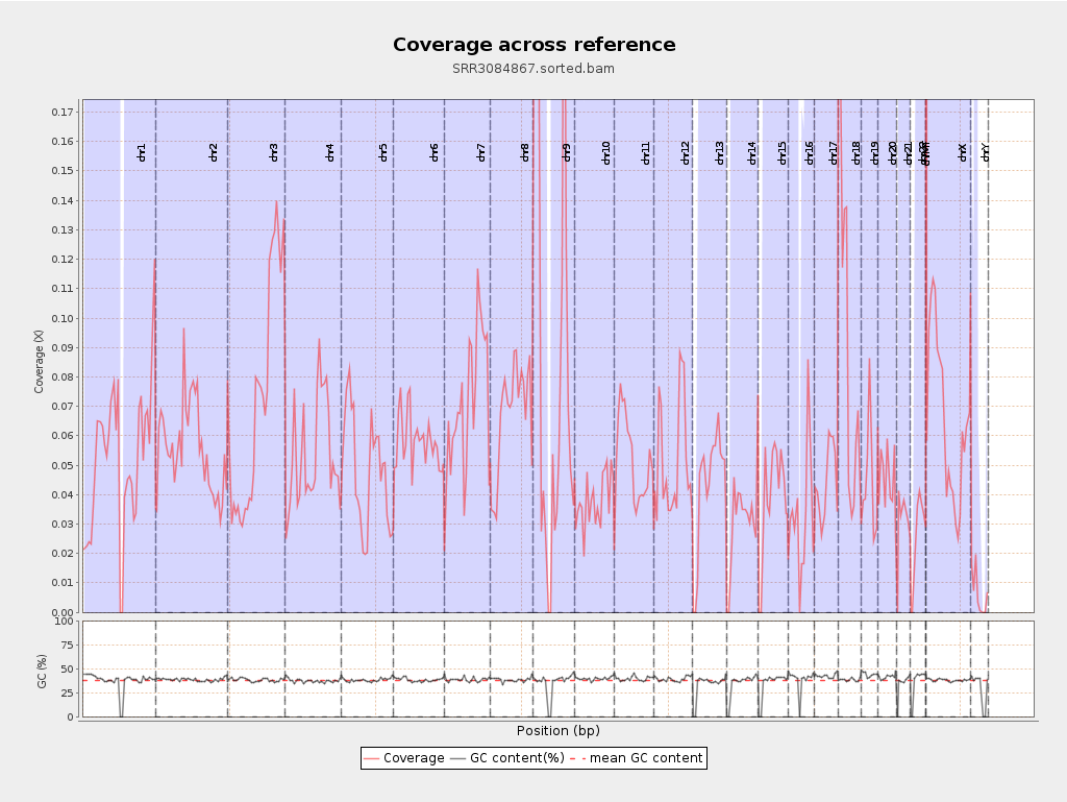
| | |
|---|---|
| General error rate | 0.84% |
| Mismatches | 1,386,869 |
| Insertions | 13,242 |
| Mapped reads with at least one insertion | 0.54% |
| Deletions | 36,394 |
| Mapped reads with at least one deletion | 1.49% |
| Homopolymer indels | 48.33% |

## 2.6. Chromosome stats

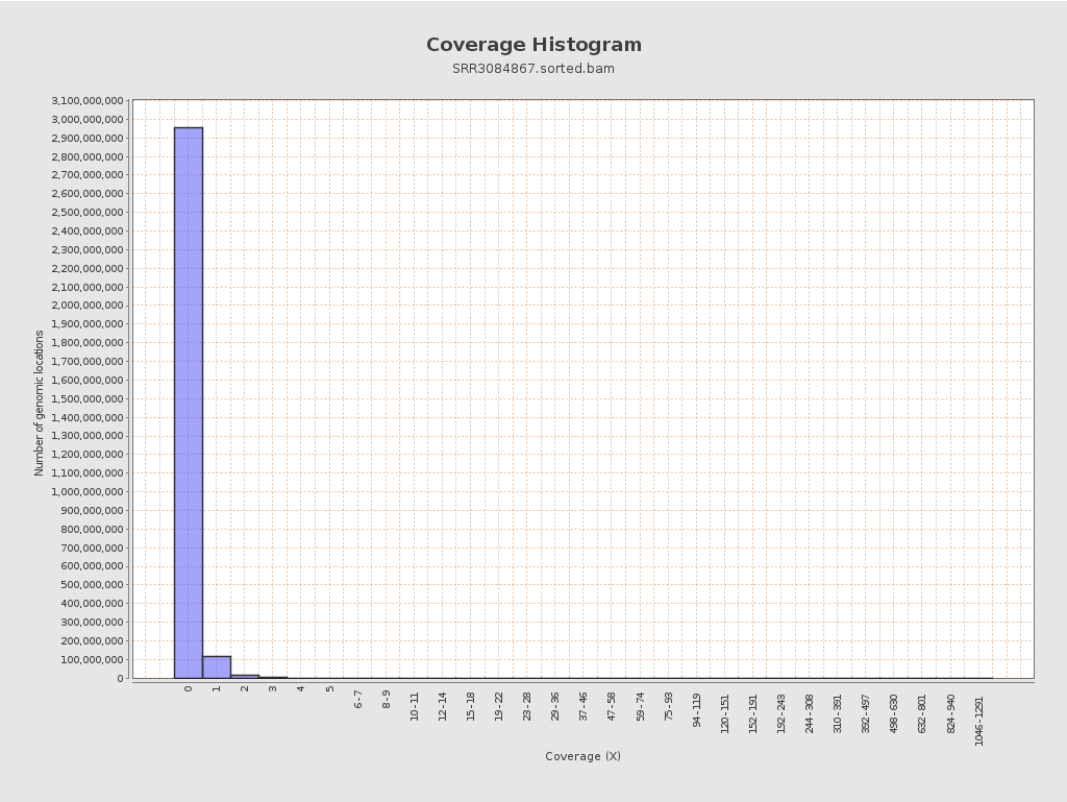
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 13036334 | 0.0523 | 0.6434 |
| chr2 | 243199373 | 13518322 | 0.0556 | 0.4299 |
| chr3 | 198022430 | 14290663 | 0.0722 | 0.3097 |
| chr4 | 191154276 | 10221488 | 0.0535 | 0.2687 |
| chr5 | 180915260 | 8696534 | 0.0481 | 0.2575 |
| chr6 | 171115067 | 9970829 | 0.0583 | 0.2864 |
| chr7 | 159138663 | 11252630 | 0.0707 | 0.4532 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9872748 | 0.0675 | 0.8801 |
| chr9 | 141213431 | 13152689 | 0.0931 | 0.4677 |
| chr10 | 135534747 | 5156103 | 0.038 | 0.2964 |
| chr11 | 135006516 | 7017156 | 0.052 | 0.3427 |
| chr12 | 133851895 | 6888387 | 0.0515 | 0.2632 |
| chr13 | 115169878 | 5000520 | 0.0434 | 0.2374 |
| chr14 | 107349540 | 3239616 | 0.0302 | 0.2113 |
| chr15 | 102531392 | 3944198 | 0.0385 | 0.2238 |
| chr16 | 90354753 | 2856731 | 0.0316 | 0.2284 |
| chr17 | 81195210 | 3690256 | 0.0454 | 0.2535 |
| chr18 | 78077248 | 7229576 | 0.0926 | 0.6908 |
| chr19 | 59128983 | 2740654 | 0.0464 | 0.4148 |
| chr20 | 63025520 | 2885079 | 0.0458 | 0.25 |
| chr21 | 48129895 | 1502511 | 0.0312 | 0.2171 |
| chr22 | 51304566 | 1319633 | 0.0257 | 0.1795 |
| chrMT | 16571 | 66169 | 3.9931 | 2.7779 |
| chrX | 155270560 | 10309372 | 0.0664 | 0.3199 |
| chrY | 59373566 | 381224 | 0.0064 | 0.2063 |

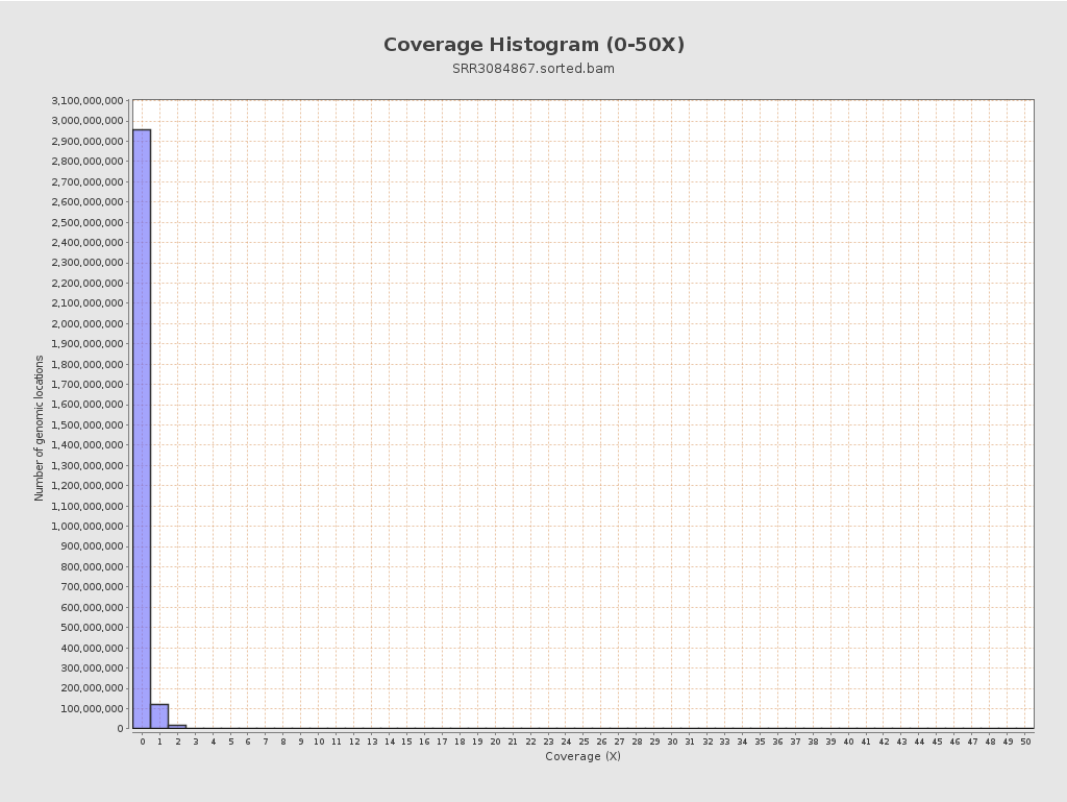
# 3. Results : Coverage across reference



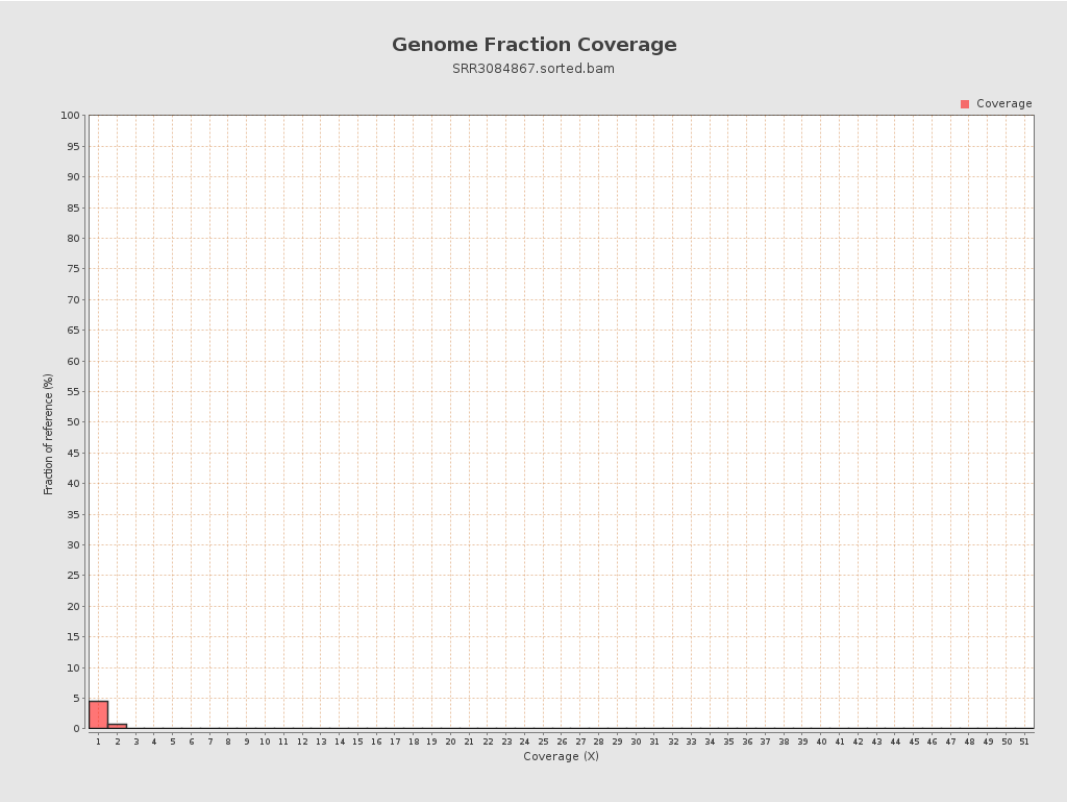
# 4. Results : Coverage Histogram



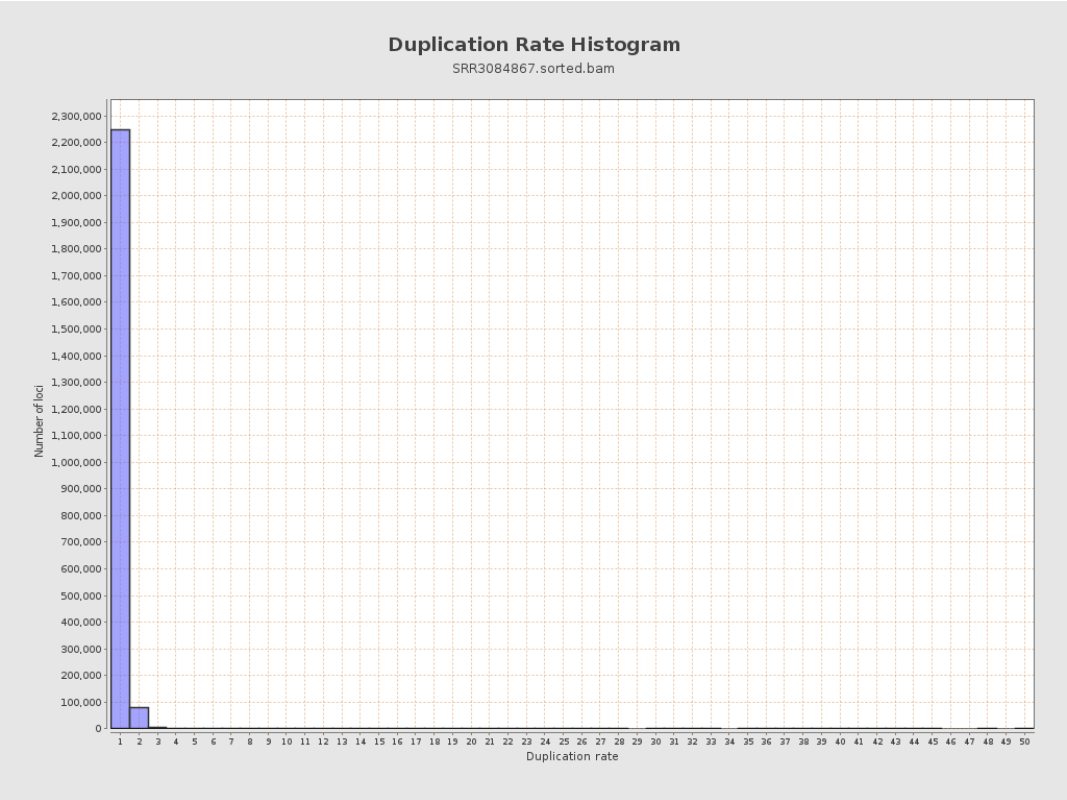
# 5. Results : Coverage Histogram (0-50X)



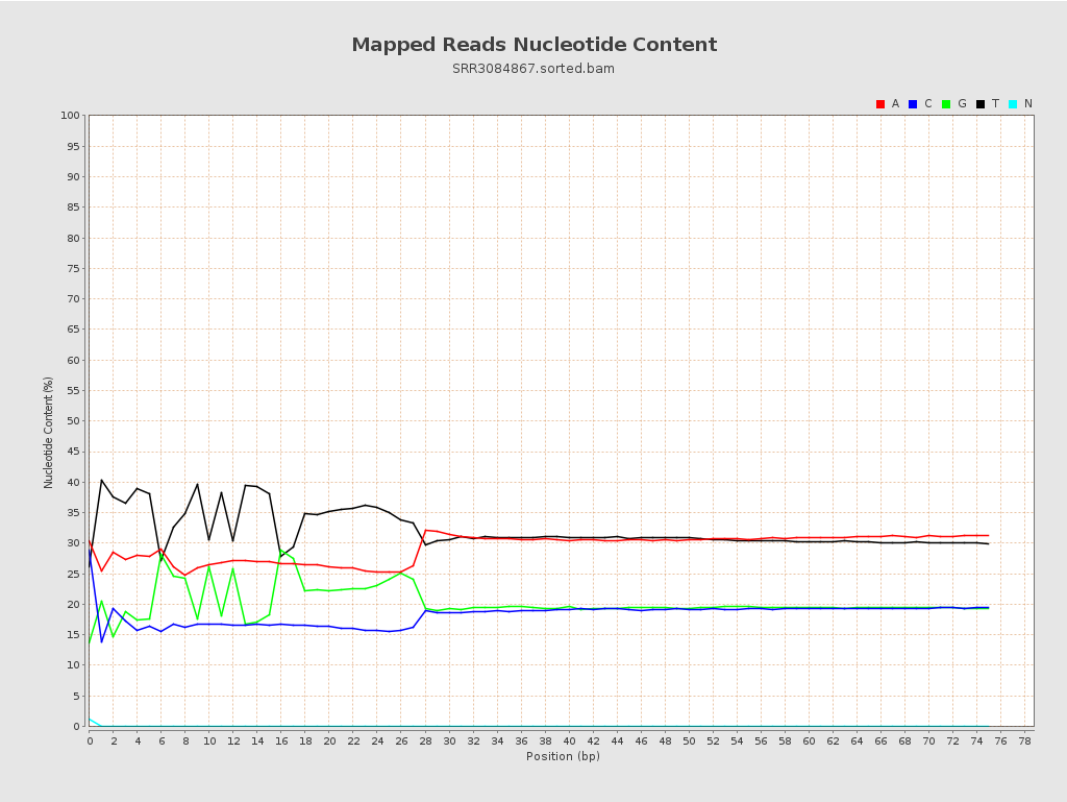
# 6. Results : Genome Fraction Coverage



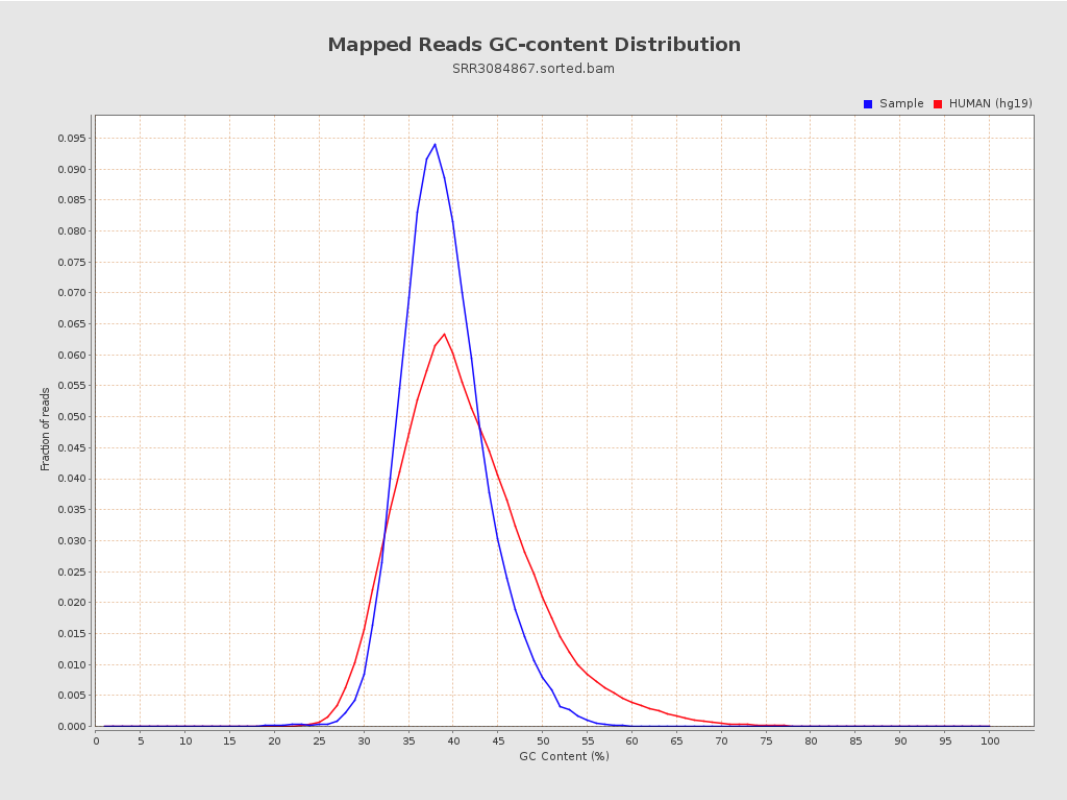
# 7. Results : Duplication Rate Histogram



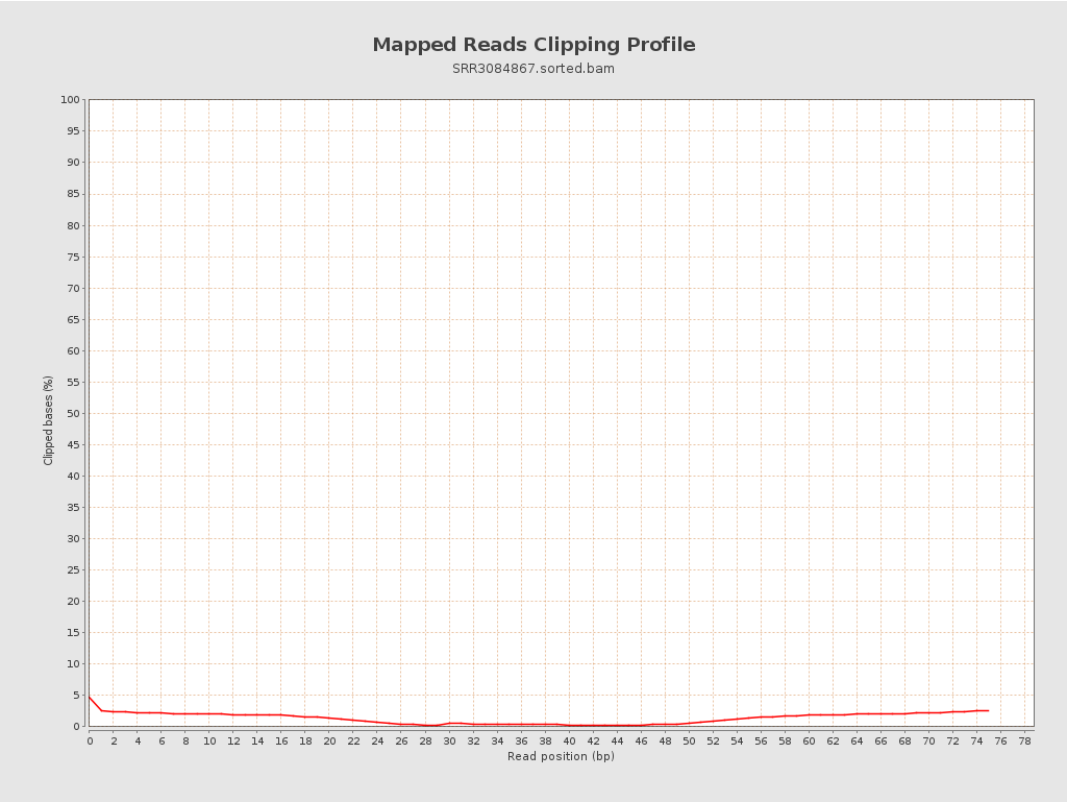
# 8. Results : Mapped Reads Nucleotide Content



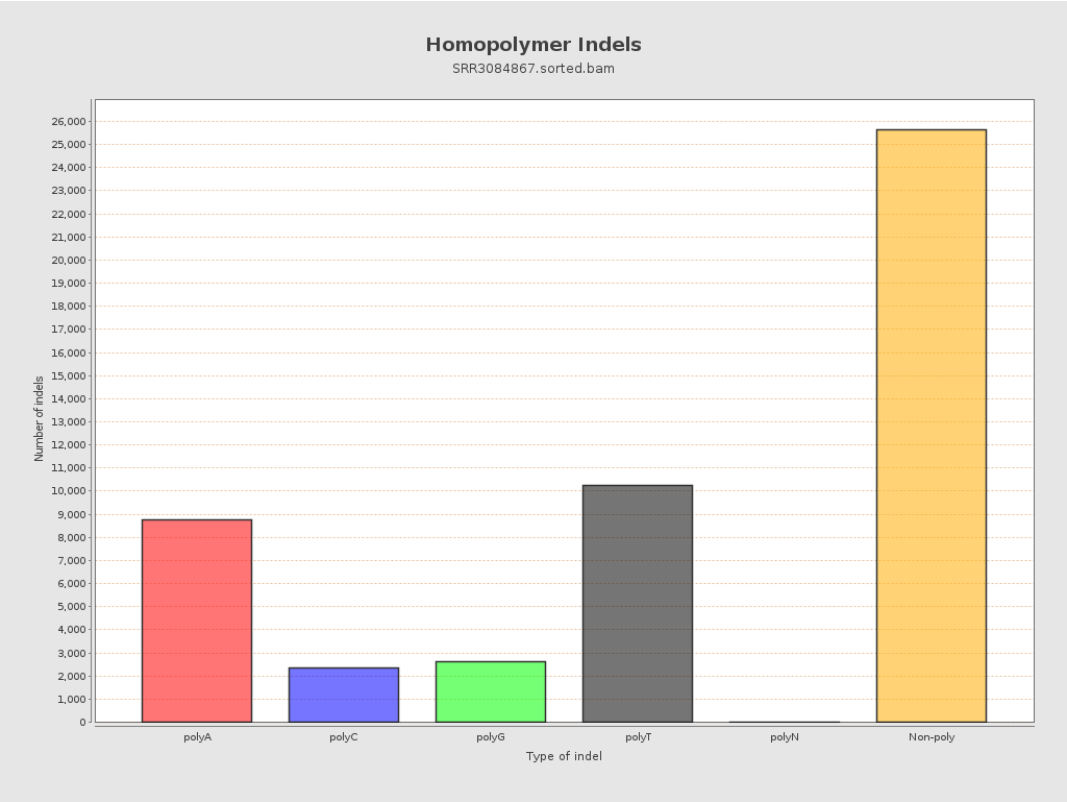
# 9. Results : Mapped Reads GC-content Distribution



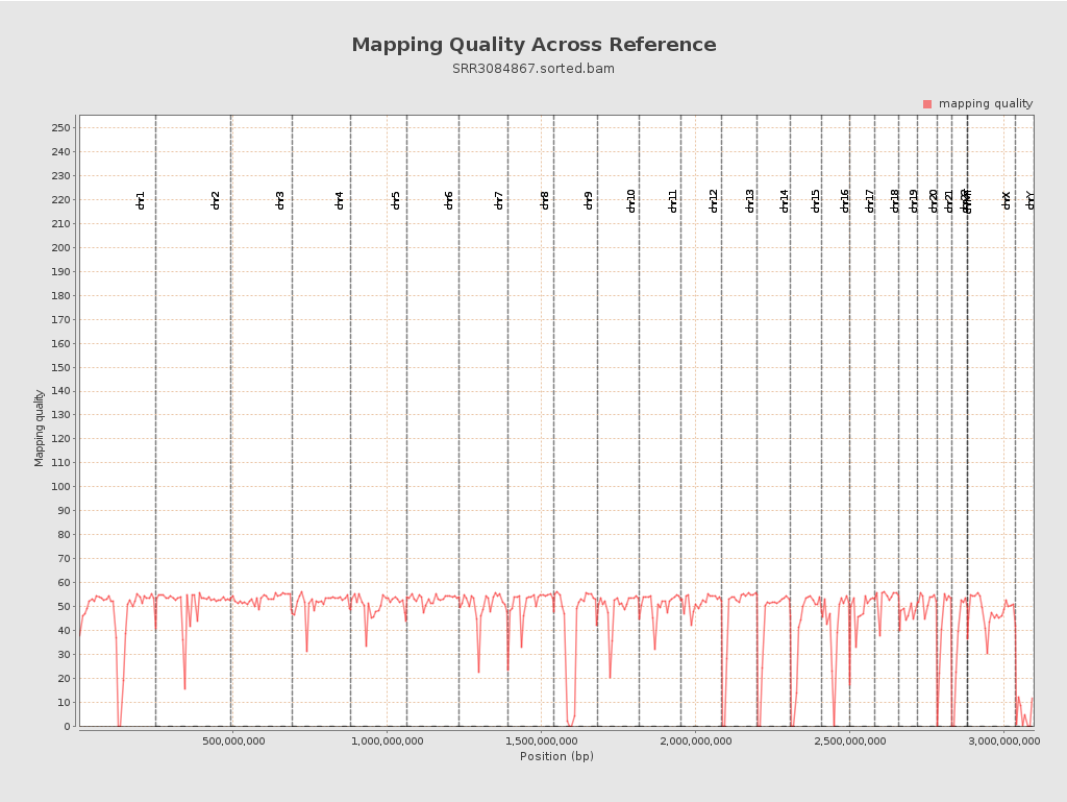
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram